

FIGURE 1A  
TRX1 Light Chain

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ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTC TGG GTT CCA GGC TCC ACT GGT GAC ATT GTG ATG ACC CAA TCT CCA GAT TCT TTG
M E T D T I L L W V L L L W V P G S T G D I V M T Q S P D S L
<-----Leader-----> <-----FR1----->
GCT GTG TCT CTA GGT GAG AGG GCC ACC ATC AAC TGC AAG GCC AGC CAA AGT GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAT CAA CAG
A V S L G E R A T I N C K A S Q S V D Y D G D S Y M N W Y Q Q
<-----CDR1-----> <----->
AAA CCA GGA CAG CCA CCC AAA CTC CTC ATC TAT GTT GCA TCC AAT CTA GAG TCT GGG GTC CCA GAC AGG TTT AGT GGC AGT GGG TCT GGG ACA
K P G Q P P K L L I Y V A S N L E S G V P D R F S G S G S T
<-----FR2-----> <-----CDR2-----> <-----FR3----->
GAC TTC ACC CTC ATC AGT TCT CTG CAG GCG GAG GAT GTT GCA GTC TAT TAC TGT CAG CAA AGT CTT CAG GAC CCT CCG ACG TTC GGT GGA
D F T L T I S S L Q A E D V A V Y Y C Q Q S L Q D P P T F G G
<-----> <-----CDR3-----> <----->
GGT ACC AAG GTG GAA ATC AAA CGA ACT GTG GCT GCA CCA TCT TTC ATC TTC CCG CCA TCT GAT GAG CAG TTG AAA TCT GGA ACT GCC TCT
G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
<-----FR4-----> <-----Constant----->
GTT GTG TGC CTG ATC AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT
V V C L L N F Y P R E A K V Q W K V D N A L Q S G N S Q E S
<----->
GTC ACA GAG CAG GAC AGC AAG GAC ACC TAC AGC CTC AGC ACC CTG AGC CTG AGC AAA GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC
V T E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A
<----->
TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TAG
C E V T H Q G L S S P V T K S F N R G E C *
<----->
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**FIGURE 1B**  
**TRX1 Light Chain Nucleic Acid Sequence**

ATGAGACAGACAAATCCTGCTATGGGTGCTGCTGCTGCTGGGTCCAGGCTCCACTGGTGACAT  
TGTGATGACCCAAATCTCCAGATTCTTTGGCTGTGCTCTAGGTGAGAGGGCCACCATCAACTGCAAG  
GCCAGCCAAAGTGTGATTATGATGGTGATAGTTATATGAAGTGGTATCAACAGAAACCAGGACAG  
CCACCCAAACTCCTCATCTATGTTGCATCCAAATCTAGAGTCTGGGTCCCAGACAGGTTTAGTGG  
CAGTGGGTCTGGGACAGACTTCACCCCTCACCATCAGTTCTCTGCAGGCGGAGGATGTTGCAGTCT  
ATTACTGTCAGCAAAAGTCTTCAGGACCCCTCCGACGTTTCGGTGGAGGTACCAAGGTGGAAATCAA  
CGAACTGTGGCTGCACCATCTGTCTTCTCCGCCCATCTGATGAGCAGTTGAAATCTGGAACT  
GCCTCTGTTGTGCCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGAT  
AACGCCCTCCAAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTA  
CAGCCTCAGCACACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCG  
AAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

**FIGURE 1C**  
**TRX1 Light Chain Amino Acid Sequence with CDRs Highlighted**

**With leader sequence:**

METDTILLWVLLWVPGSTGDI VMTQSPDLSAVSLGERATINCKASQSVDYDGD SYMNWYQQKPG  
QPPKLLIYVASNLESGVPDRFSGSGGTDFTLTISSLQAEDVAVYCCQQSLQDPPPTFGGGTKVEIKR  
TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL  
SSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

**Without leader sequence:**

DIVMTQSPDLSAVSLGERATINCKASQSVDYDGD SYMNWYQQKPGQPPKLLIYVASNLESGVPDR  
FSGSGGTDFTLTISSLQAEDVAVYCCQQSLQDPPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGT  
ASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEV  
THQGLSPVTKSFNRGEC

**FIGURE 1D**  
**TRX1 Heavy Chain**

```
ATG GAA TGG ATC TGG ATC TTT CTC CTC ATC CTG TCA GGA ACT CGA GGT GTC CAG TCC CAG GTT CAG CTG GTG CAG TCT GGA GCT GAA GTG AAG
M E W I W I F L L I L S G T R G V Q S Q V Q L V Q S G A E V K
<-----Leader----->
AAG CCT GGG GCT TCA GTG AAG GTG TCC TGT AAG GCT TCT GGA TAC ACA TTC ACT GCC TAT TAT ATA AGC TGG GTG AGG CAG GCA CCT GGA CAG
K P G A S V K V S C K A S G Y T F T A Y V I S W V R Q A P G Q
<-----FR2----->
GGC CTT GAG TGG ATG GGA GAG ATT TAT CCT GGA AGC GGT AGT AGT TAT TAT AAT GAG AAG TTC AAG GGC AGG GTC ACA ATG ACT AGA GAC ACA
G L E W M G E I Y P G S G S Y Y N E K F K G R V T M T R D T
<-----CDR2----->
TCC ACC AGC ACA GTC TAC ATG GAA CTC AGC AGC CTG AGG TCT GAG GAC ACT GCG GTC TAT TAC TGT GCA AGA TCC GGG GAC GGC AGT CGG TTT
S T S T V Y M E L S S L R S E D T A V Y Y C A R S G D G S R F
<-----FR3----->
GTT TAC TGG GGC CAA GGG ACA CTA GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC
V Y W G Q G T L V T V S S A S T K G P S V F P L A P S S K S T
<-----FR4----->
TCT GGG GGC ACA CCG GCC CTG GGC TGC CTG AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC
S G G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G
<----->
GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC
V H T F P A V L Q S S G L Y S L S S V V T V P S S L G T Q T
<----->
TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG
Y I C N V N H K P S N T K V D K K V E P K S C D K T H T C P P
<----->
TGC CCA GCA CCT GAA CTC GCG GGG GCA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CCG ACC CCT GAG GTC
C P A P E L A G A P S V F L F P P K P K D T L M I S R T P E V
<----->
ACA TGC GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG
T C V V V D V S H E D P E V K F N W Y V D G V E V H N A K T K
<----->
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App No.: Not Yet Assigned  
Inventor: Dawn Windsor-Hines et al.  
Title: INDUCING TOLERANCE IN PRIMATES

Docket No.: TLN-022

CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC  
P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y K C  
-----

AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC  
K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P  
-----

CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC  
P S R D E L T K N Q V S L T C L V K G F Y P S D I A V E W E S  
-----

AAT GGG CAG CCG GAG AAC TAC AAG ACC ACG CCT CCG GTG CTG GAC TCC GAC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG  
N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K  
-----

AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG  
S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P  
-----

GGT AAA TGA  
G K \*  
----->

**FIGURE 1E**  
**TRX1 Heavy Chain Nucleic Acid Sequence**

ATGGAATGGATCTGGATCTTCTCCTCATCCTGTCTCAGGAACCTCGAGGTGTCCAGTCCCAGGTTCCAGCTGGTGCA  
GTCTGGAGCTGAAGTGAAGACCTGGGGCTTCAGTGAAGGTGTCCTGTAAAGGCTTCTGGATACACATTCACCT  
GCCATGTTATAAGCTGGTGAGGCAGGCACCTGGACAGGGCCTTGAGTGGATGGGAGAGATTTATCCTGGAA  
GGGTAGTAGTTATTATATGAGAAAGTTCAAGGCGAGGTCACAATGACTAGAGACACATCCACCGACACAGTC  
TACATGGAACCTCAGCAGCCTGAGGTCTGAGGACACTGCGGTCTATTACTGTGCAAGATCCGGGACGGCAGTC  
GGTTGTTTACTGGGCCAAGGACACTAGTCACAGTCTCCTCAGCCTCCACCAAGGGCCCCATCGGTCTTCCC  
CCTGGCACCTCCTCCAGAGCACCTCTGGGGCACAGCGGCCCTGGCTGCCCTGGTCAAGGACTACTTCCC  
CGAACCGGTGACGGTGTCTGGAACCTCAGCGGCCCTGACCAAGCGGTGCACACCTTCCCCTGCTCCTACA  
GTCCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCCTCCAGCAGCTTGGCACCCAGACCTACATC  
TGCAACGTGAATCACAAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCCAATCTTGTGACAAACTCA  
CACATGCCACCGTGCCAGCACCTGAACCTCGCGGGGCACCGTCAAGTCTTCTTCCCCCAAAACCCCAAG  
GACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGACGTGAGCCACGAAAGACCCCTGAG  
GTCAAGTTCAACTGTTACGTGGACGGCGTGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTAC  
AACAGCACGTACCGTGTGTCAGCGTCTCACCGTCTGCACCAAGACTGGCTGAATGGCAAGGAGTACAAGT  
GCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAGCCAAAGGGCAGCCCCGAG  
AACCACAGGTGTACACCCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGGTACGCTGACCTGCCTGG  
TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGCAGCCGGAGAACAACTACAAGA  
CCACGCCCTCCGTGCTGACTCCGACGGCTCCTTCTCCTCTACAGCAAGCTCACCGTGGACAAAGCAGGTG  
GCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAGAGCCTC  
TCCCTGTCTCCGGGTAAATGA

**FIGURE 1F**  
**TRX1 Heavy Chain Amino Acid Sequence with CDRs Highlighted**

**With leader sequence:**

MEWIWIFLLILSGTRGVQSQVLVQSGAEVKPGASVKVCKASGYTFT**AYVISWVRQAPGQGLEW**  
**MGEIYPGSGSSYYNEKFKGR**VTMTTRDTSTSTVYMELSSLRSEDTAVYCAR**SGDGS****RFVYWGQG**  
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG  
LYSLSSVWTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTLMIS  
RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKA  
LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGS  
FFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

**Without leader sequence:**

QVQLVQSGAEVKPGASVKVCKASGYTFT**AYVISWVRQAPGQGLEWMGEIYPGSGSSYYNEKF**  
**KGR**VTMTTRDTSTSTVYMELSSLRSEDTAVYCAR**SGDGS****RFVYWGQ**GLTVTVSSASTKGPSVFPLA  
PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPSSSLGTQTYICNVNH  
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV  
DGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS  
RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVM  
HEALHNHYTQKSLSLSPGK

**FIGURE 2A**

**TRX1 Light Chain**

```
ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTC TGG GTT CCA GGC TCC ACT GGT GAC ATT GTG ACC CAA TCT CCA GAT TCT TTG
M E T D T I L L L W V L L L W V P G S T G D I V M T Q S P D S L
-----Leader----->
GCT GTG TCT CTA GGT GAG AGG GCC ACC ATC AAC TGC AAG GCC AGC CAA ACT GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAT CAA CAG
A V S L G E R A T I N C K A S Q S V D Y D G D S Y M N W Y Q Q
-----CDR1----->
AAA CCA GGA CAG CCA CCC AAA CTC CTC ATC TAT GTT GCA TCC AAT CTA GAG TCT GGG GTC CCA GAC AGG TTT AGT GGC AGT GGG TCT GGG ACA
K P G Q P P K L L I Y V A S N L E S G V P D R F S G S G S G T
-----PR2----->-----CDR2----->-----FR3-----
GAC TTC ACC CTC ACC ATC AGT TCT CTG CAG GCG GAG GAT GTT GCA GTC TAT TAC TGT TGT CAG CAA AGT CTT CAG GAC CCT CCG ACG TTC GGT GGA
D F T L T I S S L Q A E D V A V Y Y C Q Q S L Q D P P T F G G
-----CDR3----->
GGT ACC AAG GTG GAA ATC AAA CGA ACT GTG GCT GCA CTA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG CAG TTG AAA TCT GGA ACT GCC TCT
G T K V E I K R T V A A L S V F I F P P S D E Q L K S G T A S
-----PR4----->-----Constant-----
GTT GTG TGC CTG ATC AAT AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT
V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S
-----
GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC
V T E Q D S K D S T Y S L S S T L T L T L S K A D Y E K H K V Y A
-----
TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TAG
C E V T H Q G L S S P V T K S F N R G E C *
----->
```



**FIGURE 2B**

**TRX1 Light Chain Nucleic Acid Sequence**

ATGGAGACAGACAACTCTGCTATGGTGCTGCTGCTCTGGGTTCCAGGCT  
CCACTGGTGACATTGTGATGACCCAATCTCCAGATTCTTTGGCTGTGCTCTA  
GGTGAGAGGCCACCATCAACTGCAAGGCCAGCCAAAGTGTGATTATGATG  
GTGATAGTTATATGAACTGGTATCAACAGAAACCAGGACAGCCACCCAACT  
CCTCATCTATGTTGCATCCAATCTAGAGTCTGGGTCCTCCAGACAGGTTTAGT  
GGCAGTGGGTCTGGGACAGACTTCACCCCTCACCATCAGTTCTCTGCAGGCGG  
AGGATGTTGCAGTCTATTACTGTCAAGCAAAGTCTTCAGGACCCCTCCGACGTT  
CGGTGGAGGTACCAAGGTGGAAATCAAACGAACCTGTGGCTGCACATCTGTC  
TTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGT  
GTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG  
GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGAC  
AGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCA  
GACTACGAGAAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGA  
GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

## **FIGURE 2C**

### **TRX1 Light Chain Amino Acid Sequence with CDRs Highlighted**

With leader sequence:

METDTILLWVLLLVWVPGSTGDIVMTQSPDSLAVSLGERATINCKASQSVDYDGD SYMNNWYQQKPGQPPK  
LLIYVASNLES GVPDRFSGSGTDFTLTISSLQAEDVAVYYCQQSLQDPP TFGGGTKVEIKRTVAALS VFIF  
PPSDEQLKSGTASVVC LLNMFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSTLTLSKADYEKH  
KVYACEVTHQGLSSPVTKSFNRGEC

Without leader sequence:

DIVMTQSPDSLAVSLGERATINCKASQSVDYDGD SYMNNWYQQKPGQPPKLLIYVASNLES GVPDRFSGSG  
SGTDFTLTISSLQAEDVAVYYCQQSLQDPP TFGGGTKVEIKRTVAALS VFIFPPSDEQLKSGTASVVC LLN  
FYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF  
NRGEC

**FIGURE 2D**

**TRX1 Heavy Chain  
(aglycosyl)**

```
ATG GAA TGG ATC TGG ATC TTT CTC CTC ATC CTG TCA GGA ACT CGA GGT GTC CAG TCC CAG GTT CAG CTG GTG CAG TCT GGA GCT GAA CTG AAG
M E W I W I F L L I L S G T R G V Q S Q V Q L V Q S G A E V K
<-----Leader-----> <-----FR1----->
AAG CCT GGG GCT TCA GTG AAG GTG TCC TGT AAG GCT TCT GGA TAC ACA TTC ACT GCC TAT GTT ATA AGC TGG GTG AGG CAG GCA CCT GGA CAG
K P G A S V K V S C K A S G Y T F T A Y V I S W V R Q A P G Q
-----CDR1-----> <-----FR2----->
GGC CTT GAG TGG ATG GGA GAG ATT TAT CCT GGA AGC GGT AGT AGT TAT TAT AAT GAG AAG TTC AAG GGC AGG GTG ACA ATG ACT AGA GAC ACA
G L E W M G E I Y P G S G S S Y Y N E K F K G R V T M T R D T
-----CDR2-----> <-----FR3----->
TCC ACC AGC ACA GTC TAC ATG GAA CTC AGC AGC CTG AGG TCT GAG GAC ACT GCG GTC TAT TAC TGT GCA AGA TCC GGG GAC GGC AGT CGG TTT
S T S T V Y M E L S S L R S E D T A V Y Y C A R S G D G S R F
-----CDR3-----> <-----FR4----->
GTT TAC TGG GGC CAA GGG ACA CTA GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC
V Y W G Q G T L V T V S S A S T K G P S V F P L A P S S K S T
-----Constant-----> <-----FR5----->
TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG AAG GAC TAC TTC CCC GAA CCG GTG AGC GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC
S G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G
-----FR6-----> <-----FR7----->
GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC
V H T F P A V L Q S S G L Y S L S S V V T V P S S L G T Q T
-----FR8-----> <-----FR9----->
TAT ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG
Y I C N V N H K P S N T K V D K K V E P K S C D K T H T C P P
-----FR10-----> <-----FR11----->
TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC
C P A P E L L G G P S V F L F P P K P K D T L M I S R T P E V
-----FR12-----> <-----FR13----->
ACA TGC GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG
T C V V V D V S H E D P E V K F N W Y V D G V E V H N A K T K
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App No.: Not Yet Assigned  
Inventor: Dawn Windsor-Hines et al.  
Title: INDUCING TOLERANCE IN PRIMATES

Docket No.: TLN-022

CCG CGG GAG GAG CAG TAC GCC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC  
P R E E Q Y A S T Y R V V S V L T V L H Q D W L N G K E Y K C

AAG GTC TTC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC  
K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P

CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC  
P S R D E L T K N Q V S L T C L V K G F Y P S D I A V E W E S

AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG  
N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K

AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG  
S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P

GGT AAA TGA  
G K \*  
----->

FIGURE 2E

TRX1 aglycosyl mut Heavy Chain Nucleic Acid Sequence

ATGGAATGGATCTGGATCTTTCTCCTCATCCTGTGTCAGGAACGAGGTGTCCAGTCCCAGGTTCA  
GCTGGTGAGTCTGGAGCTGAAGTGAAGAACCTGGGGCTTCAGTGAAGGTGTCCTGTAAAGGCT  
TCTGGATACACATTCACTGCCTATGTTATAAGCTGGGTGAGGCAGGCACCTGGACAGGGCCTTGA  
GTGGATGGGAGAGATTTATCCTGGAAAGCGGTAGTAGTTATTATAATGAGAAGTTCAAGGGCAGGG  
TCACAACTGACTAGAGACACATCCACCAGCACAGTCTACATGGAACCTCAGCAGCCTGAGGTCTGAG  
GACACTGCGGTCTATTACTGTGCAAGATCCGGGACGGCAGTCGGTTTGTTTACTGGGGCCAAAG  
GGACACTAGTCACAGTCTCCTCAGCCTCCACCAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCC  
TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGTGCTGCTCAAGGACTACTTCCCCCGAAC  
CGGTGACGGTGTGCGTGAACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGGTGTCCT  
ACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC  
AGACCTACATCTGCAACGTGAATCACAAAGCCCCAGCAACACCAAGGTGGACAAAGATTGAGCCC  
AAATCTTGTGACAAAACTCACACATGCCACCCGTGCCCAGCACCTGAACTCCTGGGGGACCGTC  
AGTCTTCTCTTCCCCCAAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATG  
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG  
GAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACGCCAGCACGTACCGTGTGTGTC  
GCGTCTCACCGTCTGCACCCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAA  
CAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCCAC

App No.: Not Yet Assigned

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Inventor: Dawn Windsor-Hines et al.

Title: INDUCING TOLERANCE IN PRIMATES

AGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGAGCCTGACCTGCCT  
GGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC  
AACTACAAGACCACGCCCTCCCGTGTGCTGGACTCCGACGGCTCCTTCTCCTCTACAGCAAGCTCAC  
CGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTG  
CACAACCACTACACGCAGAGAGCCTCTCCCTGTCTCCGGGTAATGA

**FIGURE 2F**

**TRX1 Heavy Chain aglycosyl mut Amino Acid Sequence with CDRs Highlighted**

With leader sequence:

MEWIIFLLILSGTRGVQSVQLVQSGAEVKKPGASVKVCKASGYTFTAYVISWVRQAPGQGLEWMGEIYPGSGSSY  
YNEKFKGRVTMTTRDTSTSTVYMELSSLRSEDTAVYYCARSGDGRFVYWGQGLTVTVSSASTKGPSVFPLAPSSKSTS  
GGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKK  
VEPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR  
EEQYASTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELTKNQVSLTCLVK  
GFYPSDIAVEWESNGQPENNYKTTTPPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

Without leader sequence:

QVQLVQSGAEVKKPGASVKVCKASGYTFTAYVISWVRQAPGQGLEWMGEIYPGSGSSYNEKFKGRVTMTTRDTSTST  
VYMELSSLRSEDTAVYYCARSGDGRFVYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTV  
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE  
LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQ  
DWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN  
NYKTTTPPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

**FIGURE 3A**  
**TRX1 Light Chain**

```
ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTG CTG TGG GTT CCA GGC TCC ACT GGT GAC ATT GTG ATG ACC CAA TCT CCA GAT TCT TTG
M E T D T I L L L W V L L L W V P G S T G D I V M T Q S P D S L
-----Leader-----> <-----FR1----->
GCT GTG TCT CTA GGT GAG AGG GCC ACC ATC AAC TGC AAG GCC AGC CAA AGT GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAT CAA CAG
A V S L G E R A T I N C K A S Q S V D Y D G D S Y M N W Y Q Q
-----CDR1-----> <-----FR2----->
AAA CCA GGA CAG CCA CCC AAA CTC CTC ATC TAT GTT GCA TCC AAT CTA GAG TCT GGG GTC CCA GAC AGG TTT AGT GGC AGT GGG TCT GGG ACA
K P G Q P P K L L I Y V A S N L E S G V P D R F S G S G S G T
-----FR2-----> <-----CDR2-----> <-----FR3----->
GAC TTC ACC CTC ACC ATC AGT TCT CTG CAG GCG GAG GAT GTT GCA GTC TAT TAC TGT CAG CAA AGT CTT CAG GAC CCT CCG ACG TTC GGT GGA
D F T L T I S S L Q A E D V A V Y Y C Q Q S L Q D P P T F G G
-----CDR3-----> <-----FR4----->
GGT ACC AAG GTG GAA ATC AAA CGA ACT GTG GCT GCA CTA TCT TTC ATC TTC CCG CCA TCT GAT GAG CAG TTG AAA TCT GGA ACT GCC TCT
G T K V E I K R T V A A L S V F I F P P S D E Q L K S G T A S
-----FR4-----> <-----Constant----->
GTT GTG TGC CTG CTG AAT AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT
V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S
GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC AGC CTC AGC AGC ACC CTG AGC AAA GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC
V T E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A
TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TAG
C E V T H Q G L S S P V T K S F N R G E C *
----->
```



**FIGURE 3B**  
**TRX1 Light Chain Nucleic Acid Sequence**

ATGAGACAGACAAATCCTGTCTATGGGTGCTGTCTGTGGTTCCAGGCTCCACTGGTGACAT  
TGTGATGACCCAAATCTCCAGATTCTTTGGCTGTCTCTAGGTGAGAGGGCCACCATCAACTGCAAGGCCAGCC  
AAAGTGTGATTATGATGGTGATAGTTATATGAACCTGGTATCAACAGAAACCAAGGACAGCCACCCAAACTCCT  
CATCTATGTTGCATCCAATCTAGAGTCTGGGGTCCCAGACAGGTTTAGTGG  
CAGTGGGTCTGGGACAGACTTCACCCCTCACCATCAAGTTCTCTGCAGGCGGAGGATGTTGCAGTCT  
ATTA CTGT CAGCAAAGTCTTCAGGACCCCTCCGACGTTCTGGTGGAGGTACCAAGGTGGAATCAAA  
CGAACTGTGGCTGCACTATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACT  
GCCTCTGTTGTGCTGTGAATACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCT  
CCAAATCGGGTAAC TCCAGGAGAGTGTCAACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCAC  
CCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAACCCATCAGGGCCTGAGC  
TCGCCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTTAG

**FIGURE 3C**  
**TRX1 Light Chain Amino Acid Sequence with CDRs Highlighted**

**With leader sequence:**

METDTILLWVLLWVPGSTGDIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNNWYQQKPG  
QPPKLLIYVASNLESGVPDRFSGSGGTDFLTISSLQAEDVAVYYCQQSLQDPPPTFGGGTKVEIKR  
TVAALSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL  
SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

**Without leader sequence:**

DIVMTQSPDSLAVSLGERATINCKASQSVDYDGDSYMNNWYQQKPGQPPKLLIYVASNLESGVPDR  
FSGSGGTDFLTISSLQAEDVAVYYCQQSLQDPPPTFGGGTKVEIKRTVAALSVFIFPPSDEQLKSGT  
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSLSTLTLSKADYEKHKVYACEV  
THQGLSSPVTKSFNRGEC

FIGURE 3D  
TRX1 Heavy Chain

```
ATG GAA TGG ATC TGG ATC TTT CTC CTC ATC CTG TCA GGA ACT CGA GGT GTC CAG TCC CAG GTT CAG CTG GTG CAG TCT GGA GCT GAA GTG AAG
M E W I W I F L L I L S G T R G V Q S Q V Q L V Q S G A E V K
-----Leader-----
AAG CCT GGG GCT TCA GTG AAG GTG TCC TGT AAG GCT TCT GGA TAC ACA TTC ACT GCC TAT GTT ATA AGC TGG GTG AGG CAG GCA CCT GGA CAG
K P G A S V K V S C K A S G Y T F T A Y V I S W V R Q A P G Q
-----FR1-----
GGC CTT GAG TGG ATG GGA GAG ATT TAT CCT GGA AGC GGT AGT AGT TAT TAT AAT GAG AAG TTC AAG GGC AGG GTG ACA ATG ACT AGA GAC ACA
G L E W M G E I Y P G S G S S Y Y N E K F K G R V T M T R D T
-----CDR2-----
TCC ACC AGC ACA GTC TAC ATG GAA CTC AGC AGC CTG AGG TCT GAG GAC ACT GGG GTC TAT TAC TGT GCA AGA TCC GGG GAC GGC AGT CGG TTT
S T S T V Y M E L S S L R S E D T A V Y Y C A R S G D G S R F
-----FR3-----
GTT TAC TGG GGC CAA GGG ACA CTA GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC
V Y W G Q G T L V T V S S A S T K G P S V F P L A P S S K S T
-----FR4-----Constant-----
TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACQ GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC
S G G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G
-----
GTG CAC ACC TTC CCG GCT CTC CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG ACC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC
V H T F P A V L Q S S G L Y S L S S V V T V P S S S L G T Q T
-----
TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAT GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG
Y I C N V N H K P S N T K V D K K V E P K S C D K T H T C P P
-----
TGC CCA GCA CCT GAA CTC GCG GGG GCA CCG TCA GTC TTC CTC TCC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTG
C P A P E L A G A P S V F L F L F P P K P K D T L M I S R T P E V
-----
ACA TGC GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTG AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG
T C V V V D V S H E D P E V K F N W Y V D G V E V H N A K T K
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App No.: Not Yet Assigned

Docket No.: TLN-022

Inventor: Dawn Windsor-Hines et al.

Title: INDUCING TOLERANCE IN PRIMATES

CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC  
P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y K C  
-----

AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC  
K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P  
-----

CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC  
P S R D E L T K N Q V S L T C L V K G F Y P S D I A V E W E S  
-----

AAT GGG CAG CCG GAG AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG  
N G Q P E N N Y K T T P P V L D S D G S F L Y S K L T V D K  
-----

AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG  
S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P  
-----

GGT AAA TGA  
G K \*  
----->

FIGURE 3E  
TRX1 Heavy Chain Nucleic Acid Sequence

ATGGAATGGATCTGGATCTTTCTCCTCATCCTGTGTCAGGAATCGAGGTGTCCAGTCC  
CAGGTTCAGCTGGTGAGTCTGGAGCTGAAGTGAAGAAGCCTGGGGCTTCAGTGA  
AGGTGCTCTAAGGCTTCTGGATACACATTCACCTGCCTATGTTATAAGCTGGGTGA  
GGCAGGCACCTGGACAGGGCCTTGAGTGGATGGAGAGATTTATCCTGGAAGCGG  
TAGTAGTTATTATAATGAGAAAGTTCAAGGGCAGGGTCACAATGACTAGAGACACATC  
CACCAGCACAGTCTACATGGAATCAGCAGCCTGAGGTCTGAGGACACTGCGGTCT  
ATTACTGTGCAAGATCCGGGGACGGCAGTCGGTTTGTTTACTGGGGCCCAAGGGACA  
CTAGTCACAGTCTCCTCAGCCTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACCC  
CTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGAC  
TACTTCCCCGAACCGGTGACGGTGTCTGTGGAATCAGGCGCCCTGACCAGCGGCG  
TGACACCTTCCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTG  
GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCA  
CAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCCAAATCTTGTGACAAA  
CTCACACATGCCCACCGTGCCCCAGCACCTGAATCGCGGGGCCACCGTCAGTCTT  
CCTCTTCCCCCAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCA  
CATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTA  
CGTGGACGGCGTGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTAC  
AACAGCACGTACCGTGTGGTCAAGCGTCTCACCGTCTCTGCACCCAGGACTGGCTGA

.App No.: Not Yet Assigned

Docket No.: TLN-022

Inventor: Dawn Windsor-Hines et al.

Title: INDUCING TOLERANCE IN PRIMATES

ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCCAGCCCCCATCGAG  
AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAACAGGTGTACACCCCTGCC  
CCCATCCCCGGGATGAGCTGACCCAAGAACCAGGTCAAGCCTGACCTGCCCTGGTCAAA  
GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGA  
ACAACTACAAGACCACGCCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCCCTCTAC  
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCT  
CCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAAGAGCCTCTCCCTGTCT  
CCGGGTAAATGA

**FIGURE 3F**  
**TRX1 Heavy Chain Amino Acid Sequence with CDRs Highlighted**

**With leader sequence:**

MEWIFLLILSGTRGVQSQVLVQSGAEVKKPGASVKVSKASGYTFT**AYVISWVRQAPGQG**LEW  
MGEI**YPGSGSSYYNEKFKGRVT**MTTRDTSTSTVYMESSLRSEDTAVYCAR**SGDGS**RFVYWGQ  
TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG  
LYSLSSVWTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTLMIS  
RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA  
LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGS  
FFLYSKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK

**Without leader sequence:**

QVQLVQSGAEVKKPGASVKVSKASGYTFT**AYVISWVRQAPGQG**LEWMGEI**YPGSGSSYYNEKF**  
**KGRVT**MTTRDTSTSTVYMESSLRSEDTAVYCAR**SGDGS**RFVYWGQGTLLTVSSASTKGPSVFPLA  
PSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSWTVPSSSLGTQTYICNVNH  
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV  
DGVEVHNAKTKPREEEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS  
RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSV  
MHEALHNHYTQKSLSLSPGK

**FIGURE 4A**  
**TRX1 Light Chain**

```
ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTC TGG GTT CCA GGC TCC ACT GGT GAC ATT GTG ATG ACC CAA TCT CCA GAT TCT TTG
M E T D T I L L W V L L L W V P G S T G D I V M T Q S P D S L
<-----Leader-----> <-----FR1----->
GCT GTG TCT CTA GGT GAG AGG GCC ACC ATC AAC TGC AAG GCC AGC CAA AGT GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAT CAA CAG
A V S L G E R A T I N C K A S Q S V D Y D G D S Y M N W Y Q Q
<-----> <-----CDR1----->
AAA CCA GGA CAG CCA CCC AAA CTC CTC ATC TAT GTT GCA TCC AAT CTA GAG TCT GGG GTC CCA GAC AGG TTT AGT GGC AGT GGG TCT GGG ACA
K P G Q P P K L L I Y V A S N L E S G V P D R F S G S G S T
<-----FR2-----> <-----CDR2-----> <-----FR3----->
GAC TTC ACC CTC ACC ATC AGT TCT CTG CAG GCG GAG GAT GTT GCA GTC TAT TAC TGT CAG CAA AGT CTT CAG GAC CCT CCG ACG TTC GGT GGA
D F T L T I S S L Q A E D V A V Y Y C Q Q S L Q D P P T F G G
<-----> <-----CDR3-----> <----->
GGT ACC AAG GTG GAA ATC AAA CGA ACT GTG GCT GCA CCA TCT TTC ATC TTC CCG CCA TCT GAT GAG CAG TTG AAA TCT GGA ACT GCC TCT
G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
<-----FR4-----> <-----Constant----->
GTT GTG TGC CTG AAT AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT
V V C L L N F Y P R E A K V Q W K V D N A L Q S G N S Q E S
<-----> <-----> <----->
GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC AGC CTC AGC AGC ACC CTG AGC AAA GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC
V T E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A
<-----> <-----> <----->
TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC GTG ACA AAG AGC TTC AAC AGG GGA GAG TGT TAG
C E V T H Q G L S S P V T K S F N R G E C *
<-----> <-----> <----->
```



**FIGURE 4B**  
**TRX1 Light Chain Nucleic Acid Sequence**

ATGGAGACAGACAAATCCTGCTATGGGTGCTGCTGCTCTGGGTTCCAGGCTCCACTGGTGACAT  
TGTGATGACCCAAATCTCCAGATTCTTTGGCTGTCTCTAGGTGAGAGGCCACCATCAACTGCAAG  
GCCAGCCAAAGTGTGATTATGATGGTGATAGTTATATGAACCTGGTATCAACAGAAACAGGACAG  
CCACCCAAACTCCTCATCTATGTTGCATCCAATCTAGAGTCTGGGTCCCAGACAGGTTAGTGG  
CAGTGGGTCTGGGACAGACTTCACCCCTCACCATCAGTTCTCTGCAGGCGGAGGATGTTGCAGTCT  
ATTACTGCAGCAAAGTCTTCAGGACCCCTCCGACGTTTCGGTGGAGGTACCAAGGTGGAAATCAAA  
CGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAC  
GCCTCTGTTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAGGTGGAT  
AACGCCCTCCAAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGCAGCAAGGACAGCACCTA  
CAGCCTCAGCACACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGG  
AAGTCACCCATCAGGGCCTGAGCTCGCCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTAG

**FIGURE 4C**  
**TRX1 Light Chain Amino Acid Sequence with CDRs Highlighted**

**With leader sequence:**

METDITLLWVLLWVPGSTGDIVMTQSPDSLAVSLGERATINCKASQSVDYDGD SYMNNWYQQKPG  
QPPKLLIYVASNLESGVPDRFSGSGGTDFLTISSLQAEDVAVYYCQQSLQDPPTFGGG TKVEIKR  
TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSL  
SSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

**Without leader sequence:**

DIVMTQSPDSLAVSLGERATINCKASQSVDYDGD SYMNNWYQQKPGPPKLLIYVASNLESGVPDR  
FSGSGGTDFLTISSLQAEDVAVYYCQQSLQDPPTFGGG TKVEIKRTVAAPSVFIFPPSDEQLKSGT  
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSTLTLSKADYEKHKVYACEV  
THQGLSPVTKSFNRGEC

**FIGURE 4D**

**TRX1 Heavy Chain  
(aglycosyl)**

```
ATG GAA TGG ATC TGG ATC TTT CTC ATC CTG TCA GGA ACT CGA GGT GTC CAG TCC CAG GTT CAG CTG GTG CAG TCT GGA GCT GAA GTG AAG
M E W I W I F L L I L S G T R G V Q S Q V Q L V Q S G A E V K
<-----Leader-----> <-----FRI----->
AAG CCT GGG GCT TCA GTG AAG GTG TCC TGT AAG GCT TCT GGA TAC ACA TTC ACT GCC TAT GTT ATA AGC TGG GTG AGG CAG GCA CCT GGA CAG
K P G A S V K V S C K A S G Y T F T A Y V I S W V R Q A P G Q
-----CDR1-----> <-----FR2----->
GGC CTT GAG TGG ATG GGA GAG ATT TAT CCT GGA AGC GGT AGT AGT TAT TAT AAT GAG AAG TTC AAG GGC AGG GTC ACA ATG ACT AGA GAC ACA
G L E W M G E I Y P G S G S S Y Y N E K F K G R V T M T R D T
-----CDR2-----> <-----FR3----->
TCC ACC AGC ACA GTC TAC ATG GAA CTC AGC AGC CTG AGG TCT GAG GAC ACT GCG GTC TAT TAC TGT GCA AGA TCC GGG GAC GGC AGT CGG TTT
S T S T V Y M E L S S L R S E D T A V Y Y C A R S G D G S R F
-----FR3-----> <-----CDR3----->
GTT TAC TGG GGC CAA GGG ACA CTA GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC
V Y W G Q G T L V T V S S A S T K G P S V F P L A P S S K S T
-----FR4-----> <-----Constant----->
TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GGC CTG ACC AGC GGC
S G G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G
-----> <----->----->
GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC
V H T F P A V L Q S S G L Y S L S S V V T V P S S L G T Q T
-----> <----->----->
TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG
Y I C N V N H K P S N T K V D K K V E P K S C D K T H T C P P
-----> <----->----->
TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC
C P A P E L L G G P S V F L F P P K P K D T L M I S R T P E V
-----> <----->----->
ACA TGC GTG GTG GAC GTG ACC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG
T C V V V D V S H E D P E V K F N W Y V D G V E V H N A K T K
```

CCG CGG GAG GAG CAG TAC GCC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC GAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC  
P R E E Q Y A S T Y R V V S V L T V L H Q D W L N G K E Y K C

AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC  
K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P

CCA TCC CGG GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC  
P S R D E L T K N Q V S L T C L V K G F Y P S D I A V E W E S

AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCG GTG CTG GAC TCC GGC GGC TCC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG  
N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K

AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG  
S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P

GGT AAA TGA  
G K \*  
----->

**FIGURE 4E**

TRX1 aglycosyl mut Heavy Chain Nucleic Acid Sequence

ATGGAATGGATCTGGATCTTTCTCCTCATCCTGTCAGGAACTCGAGGTGTCCAGTCCCAGGTTCA  
GCTGGTGCAGTCTGGAGCTGAAGTGAAGAAGCCTGGGGCTTCAGTGAAGGTGTCCTGTAAGGCT  
TCTGGATACACATTCACTGCCCTATGTTATAAGCTGGGTGAGGCAGGCACCTGGACAGGGCCTTGA  
GTGGATGGGAGAGATTTATCCTGGAAGCGGTAGTAGTTATTATAATGAGAAAGTTCAAGGGCAGGG  
TCACAATGACTAGAGACACATCCACCAGCACAGTCTACATGGAACCTCAGCAGCCTGAGGTCTGAG  
GACACTGCGGTCTATTACTGTGCAAGATCCGGGACGGCAGTCGGTTTGTCTTACTGGGGCCAAAG  
GGACACTAGTCACAGTCTCCTCAGCCTCCACCAGGGGCCCATCGGTCTTCCCCCTGGCACCCCTC  
CTCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGCTGCCCTGCTCAAGGACTACTTCCCCCGAA  
CCGGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGTGCACACCTTCCCCGGCTGTC  
CTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA  
CCCAGACCTACATCTGCAACGTGAATCACAAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAG  
CCCAAATCTTGTGACAAAACCTCACACATGCCACCCGTGCCCAGCACCTGAACCTCCTGGGGGAC  
CGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTC  
ACATGCGTGGTGGACGTGAGCCACGAAAGACCCCTGAGGTCAAAGTTCAAAGTGGTACGTGGACG  
GCGTGAGGTGCATAATGCCAAGACAAAAGCCGCGGAGGAGCAGTACGCCAGCACGTACCCGTG  
TGGTCAGCGTCCCTCACCGTCCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAAGTGCAAGGT  
CTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGGCAGCCCCCGA  
GAACCACAGGTGTACACCCCTGCCCCCATCCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGA

App No.: Not Yet Assigned  
Inventor: Dawn Windsor-Hines et al.  
Title: INDUCING TOLERANCE IN PRIMATES

Docket No.: TLN-022

CCTGCCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC  
GGAGAACTACAAGACCACGCCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCA  
AGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGA  
GGCTCTGCACAACCACTACACGCAGAGAGCCCTCTCCCTGTCTCCGGGTAATGA

**FIGURE 4F**

**TRX1 Heavy Chain aglycosyl mut Amino Acid Sequence with CDRs Highlighted**

With leader sequence:

MEWIWIFLLILSGTRGVQSQVQLVQSGAEVKKPGASVKVCKASGYTFTAYVISWVRQAPGQGLEWMGEI  
YPGSGSSYYNEKFKGRVTMTTRDTSTVYMELSSLRSEDTAVYYCARSGDGRFVYWGQGLVTVSSAS  
TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS  
LGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV  
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIE  
KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFF  
LYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK

Without leader sequence:

QVQLVQSGAEVKKPGASVKVCKASGYTFTAYVISWVRQAPGQGLEWMGEIYPGSGSSYYNEKFKGRVT  
MTRDTSTSTVYMELSSLRSEDTAVYYCARSGDGRFVYWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGT  
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTKV  
DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV  
EVHNAKTKPREEQYASTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP  
SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS  
CSVMHEALHNHYTQKSLSLSPGK

# FIGURE 5 HEAVY CHAIN

Sequence Range: 1 to 1356

10	20	30	40	50	60
CAG GTT CAA TTG GTG GAG TCT GGA GGC GTT GTA CAG CCT GGA AGG TCC CTG AGA CTC					
Q V Q L V E S G G G V V Q P G R S L R L>					
70	80	90	100	110	120
TCA TGT GCA GCT TCT GGA TTC ACT TTC AGT GAC TTT GGC ATG AAC TGG GTT CGA CAG GCT					
S C A A S G F T F S D F G M N W V R Q A>					
130	140	150	160	170	180
CCC GGG AAG GGG CTG GAA TGG GTG GCA CTG ATT TAC TAT GAT GGT AGT AAC AAG TTC TAT					
P G K G L E W V A L I Y Y D G S N K F Y>					
190	200	210	220	230	240
GCA GAC TCT GTG AAG GGT CGA TTC ACC ATC TCC AGG GAC AAT TCT AAG AAC ACC CTA TAC					
A D S V K G R F T I S R D N S K N T L Y>					
250	260	270	280	290	300
CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACA GCC GTG TAT TAC TGT GCA AAA CCC CAC					
L Q M N S L R A E D T A V Y Y C A K P H>					
310	320	330	340	350	360
TAT GAT GGT TAT TAT CAC TTC TTT GAT TCC TGG GGC CAA GGG ACA CTA GTC ACA GTC TCC					
Y D G Y Y H F F D S W G Q G T L V T V S>					
370	380	390	400	410	420
TCA GCC TCC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC AAG AGC ACC TCT					
S A S T K G P S V F P L A P S S K S T S>					
430	440	450	460	470	480
GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG					
G G T A A L G C L V K D Y F P E P V T V>					
490	500	510	520	530	540
TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC					
S W N S G A L T T S G V H T F P A V L Q S>					



550 560 570 580 590 600  
TCA GGA CTC TAC TCC CTC AGC AGC GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG  
S G L Y S L S S V V T V P S S S L G T Q>

610 620 630 640 650 660  
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG  
T Y I C N V N H K P S N T K V D K K V E>

670 680 690 700 710 720  
CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG  
P K S C D K T T H T C P P C P A P E L L G>

730 740 750 760 770 780  
GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC  
G P S V F L F P P K P K D T L M I S R T>

790 800 810 820 830 840  
CCT GAG GTC ACA TGC GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC  
P E V T C V V V D V S H E D P E V K F N>

850 860 870 880 890 900  
TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC  
W Y V D G V E V H N A K T K P R E E Q Y>

910 920 930 940 950 960  
AAC AGC ACG TAC CGT GTG GTC AGC GTG CAT ACC GTG CTC CAC CAG GAC TGG CTG AAT GGC  
N S T Y R V V S V L T V L H Q D W L N G>

970 980 990 1000 1010 1020  
AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC  
K E Y K C K V S N K A L P A P I E K T I>

1030 1040 1050 1060 1070 1080  
TCC AAA GCC AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT  
S K A K G G Q P R E P Q V Y T L P P S R D>

1090 1100 1110 1120 1130 1140  
GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC  
E L T K N Q V S L T C L V K G F Y P S D>

1150 1160 1170 1180 1190 1200

App No.: Not Yet Assigned

Docket No.: TLN-022

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ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC
I  A  V  E  W  E  S  N  G  Q  P  E  N  N  Y  K  T  T  P  P>

1210      1220      1230      1240      1250      1260
GTG CTG GAC TCC GAC GGC TCC TTC TTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG
V  L  D  S  D  G  S  F  F  L  Y  S  K  L  T  V  D  K  S  R>

1270      1280      1290      1300      1310      1320
TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC
W  Q  Q  G  G  N  V  F  S  C  S  V  M  H  E  A  L  H  N  H  Y>

1330      1340      1350
ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA
T  Q  K  S  L  S  L  S  P  G  K  *>
```

## FIGURE 6

## LIGHT CHAIN

Sequence Range: 1 to 648

			10			20			30			40				
GAC	ATC	CAG	ATG	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC	AGC	GTG	GGT	
D	I	Q	M	T	Q	S	P	S	S	L	S	A	S	V	G>	
50			60			70			80			90				
GAC	AGA	GTG	ACC	ATC	ACC	TGT	AAA	GGA	AGT	CAG	GAT	ATT	AAC	AAT	TAC	
D	R	V	T	I	T	C	K	G	S	Q	D	I	N	N	Y>	
	100			110		120			130			140				
TTA	GCC	TGG	TAC	CAG	CAG	AAG	CCA	GGT	AAG	GCT	CCA	AAG	CTG	CTG	ATC	
L	A	W	Y	Q	Q	K	P	G	K	A	P	K	L	L	I>	
	150			160		170			180			190				
TAC	AAT	ACA	GAC	ATT	TTG	CAC	ACG	GGT	GTG	CCA	AGC	AGA	TTC	AGC	GGT	
Y	N	T	D	I	L	H	T	G	V	P	S	R	F	S	G>	
	200			210		220			230			240				
AGC	GGT	AGC	GGT	ACC	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC	CTC	CAG	CCA	
S	G	S	G	T	D	F	T	F	T	I	S	S	L	Q	P>	
	250			260		270			280							
GAG	GAC	ATC	GCC	ACC	TAC	TAC	TGC	TAT	CAG	TAT	AAC	AAC	GGG	TAC	ACG	
E	D	I	A	T	Y	Y	C	Y	Q	Y	N	N	G	Y	T>	
290			300			310			320			330				
TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	CGA	ACT	GTG	GCT	GCA	CCA	
F	G	Q	G	T	K	V	E	I	K	R	T	V	A	A	P>	
	340			350		360			370			380				
TCT	GTC	TTC	ATC	TTC	CCG	CCA	TCT	GAT	GAG	CAG	TTG	AAA	TCT	GGA	ACT	
S	V	F	I	F	P	P	S	D	E	Q	L	K	S	G	T>	
	390			400		410			420			430				
GCC	TCT	GTT	GTG	TGC	CTG	CTG	AAT	AAC	TTC	TAT	CCC	AGA	GAG	GCC	AAA	
A	S	V	V	C	L	L	N	N	F	Y	P	R	E	A	K>	
	440			450		460			470			480				
GTA	CAG	TGG	AAG	GTG	GAT	AAC	GCC	CTC	CAA	TCG	GGT	AAC	TCC	CAG	GAG	
V	Q	W	K	V	D	N	A	L	Q	S	G	N	S	Q	E>	

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      490      500      510      520
AGT  GTC  ACA  GAG  CAG  GAC  AGC  AAG  GAC  AGC  ACC  TAC  AGC  CTC  AGC  AGC
S    V    T    E    Q    D    S    K    D    S    T    Y    S    L    S    S>

530      540      550      560      570
ACC  CTG  ACG  CTG  AGC  AAA  GCA  GAC  TAC  GAG  AAA  CAC  AAA  GTC  TAC  GCC
T    L    T    L    S    K    A    D    Y    E    K    H    K    V    Y    A>

      580      590      600      610      620
TGC  GAA  GTC  ACC  CAT  CAG  GGC  CTG  AGC  TCG  CCC  GTC  ACA  AAG  AGC  TTC
C    E    V    T    H    Q    G    L    S    S    P    V    T    K    S    F>

      630      640
AAC  AGG  GGA  GAG  TGT  TAG
N    R    G    E    C    *
```